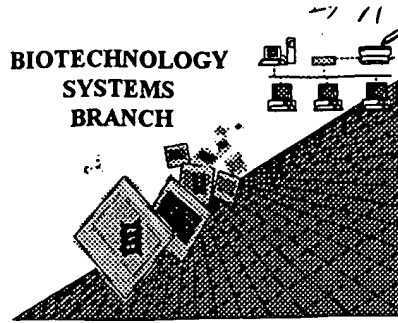


BEST AVAILABLE COPY

BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/509,449B
Source: 1648
Date Processed by STIC: 5/11/2001

RECEIVED

MAY 29 2001

TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

1648

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/509,449B

DATE: 05/11/2001
TIME: 13:46:39

Input Set : A:\ST25.txt
Output Set: N:\CRF3\05112001\I509449B.raw

3 <110> APPLICANT: Aoyagi, Katsumi
4 Ohue, Chiharu
5 Iida, Kumiko
6 Yagi, Shintaro
8 <120> TITLE OF INVENTION: Method for Measurement of Hepatitis C Virus
10 <130> FILE REFERENCE: 594.352USWO
12 <140> CURRENT APPLICATION NUMBER: 09/509,449B
13 <141> CURRENT FILING DATE: 2000-03-28
15 <150> PRIOR APPLICATION NUMBER: JP-10-216094
16 <151> PRIOR FILING DATE: 1998-07-30
18 <150> PRIOR APPLICATION NUMBER: PCT/JP99/04129
19 <151> PRIOR FILING DATE: 1999-07-30
21 <160> NUMBER OF SEQ ID NOS: 11
23 <170> SOFTWARE: PatentIn version 3.0

Does Not Comply
Corrected Diskette Needed

pp 1-2
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ERRORED SEQUENCES

317 <210> SEQ ID NO: 11
318 <211> LENGTH: 396
319 <212> TYPE: PRT
C--> 320 <213> ORGANISM: Artificial *see item 11 on Ena Summary Sheet*
322 <220> FEATURE:
323 <223> OTHER INFORMATION: Amino acid sequence coding for chimeric antigen.
325 <400> SEQUENCE: 11
327 Glu Phe Thr Lys Val Pro Val Ala Tyr Ala Ala Lys Gly Tyr Lys Val
328 1 5 10 15
331 Leu Val Leu Asp Pro Ser Val Ala Ser Thr Leu Gly Phe Gly Ala Tyr
332 20 25 30
335 Leu Ser Lys Ala His Gly Val Asn Pro Asn Ile Arg Thr Gly Ile Arg
336 35 40 45
339 Thr Val Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr Tyr Gly Lys Tyr
340 50 55 60
343 Leu Ala Asp Gly Gly Cys Ala Gly Gly Ala Tyr Asp Val Ile Gly Ser
344 65 70 75 80
347 Gly Glu Glu Val Ala Leu Ser Asn Thr Gly Glu Val Pro Phe Tyr Gly
348 85 90 95
351 Arg Ala Ile Pro Ile Glu Ala Ile Lys Gly Gly Arg His Leu Val Phe
352 100 105 110
355 Cys His Ser Lys Glu Lys Cys Asp Glu Leu Ala Ser Ala Leu Ser Gly
356 115 120 125
359 Leu Gly Leu Asn Ala Val Ala Phe Tyr Arg Gly Leu Asp Val Ser Ile
360 130 135 140
363 Ile Pro Thr Gln Gly Asp Val Val Ile Val Ser Thr Asp Ala Leu Met
364 145 150 155 160
367 Thr Gly Phe Thr Gly Asp Phe Asp Ser Val Val Asp Cys Asn Thr Cys
368 165 170 175

The types of errors shown exist throughout the Sequence Listing. Please check
a || sequences for similar errors.

RAW SEQUENCE LISTING

DATE: 05/11/2001

PATENT APPLICATION: US/09/509,449B

TIME: 13:46:39

Input Set : A:\ST25.txt

Output Set: N:\CRF3\05112001\I509449B.raw

```

371 Ile Thr Gln Gly Ser Gly Leu Val Ser Phe Ala Ser His Val Pro Tyr
372      180      185      190
375 Ile Glu Gln Gly Met Gln Leu Ser Glu Gln Phe Lys Gln Lys Ser Leu
376      195      200      205
379 Gly Leu Leu Gln Thr Ala Thr Lys Gln Ala Glu Ala Ala Ala Pro Val
380      210      215      220
383 Val Gly Thr Pro Lys Ser Arg Arg Pro Glu Gly Arg Ala Trp Ala Gln
384 225      230      235      240
387 Pro Gly Thr Ile Ile Leu Ser Gly Arg Pro Ala Val Val Pro Asp Arg
388      245      250      255
391 Glu Val Leu Tyr Gln Glu Phe Leu Glu Ala Ser Arg Ala Ala Leu Ile
392      260      265      270
395 Glu Glu Gly Gln Arg Ile Ala Glu Met Leu Lys Ser Lys Ile Gln Gly
396      275      280      285
399 Leu Leu Gln Gln Ala Ser Lys Gln Ala Gln Asp Ile Lys Ile Asp Gly
400      290      295      300
403 Thr Leu Ile Ile Pro Lys Asp Arg Arg Ser Thr Gly Lys Ser Trp Gly
404 305      310      315      320
407 Lys Pro Gly Phe Leu Ile Asp Ser Leu His Ile Asn Gln Arg Ala Val
408      325      330      335
411 Val Ala Pro Asp Lys Glu Val Leu Tyr Glu Ala Phe Asp Glu Met Glu
412      340      345      350
415 Leu Ala Met Gly Thr Asn Pro Lys Pro Glu Arg Lys Ser Lys Arg Asn
416      355      360      365
419 Thr Asn Arg Lys Pro Gln Asp Ile Lys Phe Pro Gly Ser Gly Gln Val
420      370      375      380
423 Val Gly Gly Val Tyr Leu Val Pro Arg Arg Gly Pro
424 385      390      395

```

E--> 431 6

delete at end of file

VERIFICATION SUMMARY

DATE: 05/11/2001

PATENT APPLICATION: US/09/509,449B

TIME: 13:46:40

Input Set : A:\ST25.txt

Output Set: N:\CRF3\05112001\I509449B.raw

L:108 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3
L:124 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4
L:137 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5
L:153 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6
L:169 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7
L:181 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8
L:193 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9
L:206 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10
L:320 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:11
L:431 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:11

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/509,449B

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.

- 4 Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) . Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.

- 8 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X:
 (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
 This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

- 9 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) <210> sequence id number
 <400> sequence id number
 000

- 10 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

- 11 Use of "Artificial" Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.
(NEW RULES) Valid response is Artificial Sequence.

- 12 Use of <220>Feature Sequence(s) are missing the <220>Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"
 Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)

- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.